

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 6, 2001, 13:35:37 ; Search time 62.8 Seconds
(without alignments)
268.371 Million cell updates/sec

Title: US-09-668-482-2

Perfect score: 2563

Sequence: 1 MGLYTLVFLCTIVLPVLL.....GPTIYPVDNIPTKFTSYVRN 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2563	100.0	492	1	CP26_BRARE
2	1741	67.9	497	1	O43174 brachydanio
3	1734	67.7	497	1	CP26_MOUSE
4	552.5	21.6	472	1	CP01_ARATH
5	481	18.8	464	1	CP85_LYCES
6	450	17.6	490	1	CP83_ARATH
7	375	14.6	519	1	CP81_MAIZE
8	363	14.2	492	1	CP16_MCTU
9	350.5	13.7	518	1	CP3R_ONCMY
10	343.5	13.4	501	1	CP36_RABIT
11	339.5	13.2	490	1	CP09_HUMAN
12	339.5	13.2	490	1	CP04_HUMAN
13	333	13.0	503	1	CP39_RAT
14	331	12.9	505	1	CP48_DROME
15	330.5	12.9	459	1	CPXN_ANASP
16	330.5	12.9	520	1	CP84_ARATH
17	329	12.8	504	1	CP3G_MOUSE
18	328.5	12.8	530	1	CP51_YEAST
19	326	12.7	503	1	CP3T_PIG
20	326	12.7	503	1	CP51_PIG
21	324.5	12.7	503	1	CP33_HUMAN
22	324.5	12.7	507	1	CP3S_BOVIN
23	324	12.6	511	1	CP45_RABIT
24	323.5	12.6	492	1	CP11_DROME
25	323.5	12.6	508	1	CP48_RAT
26	322.5	12.6	500	1	CP0B_RAT
27	322.5	12.6	503	1	CP0C_RAT
28	322.5	12.6	503	1	CP3C_CANFA
29	320	12.5	502	1	CP3E_CAVPO
30	320	12.5	507	1	CP34_HUMAN
31	318	12.4	503	1	CP4E_DROME
32	317.5	12.4	496	1	CP51_HUMAN
33	317	12.4	503	1	C7B1_THLAR
					CP51_RAT

34	315.5	12.3	489	1	CP26_CANFA
35	315	12.3	499	1	C719_SOYEN
36	315	12.3	511	1	CP47_RABIT
37	314.5	12.3	503	1	CP3F_CAVPO
38	314	12.3	504	1	CP32_RAT
39	314	12.3	510	1	C4DK_DROME
40	313.5	12.2	501	1	C4D2_DROME
41	311.5	12.2	490	1	C7DB_LOTJA
42	311.5	12.2	490	1	CP0J_HUMAN
43	311.5	12.2	502	1	CP35_HUMAN
44	311.5	12.2	504	1	CP3B_MOUSE
45	311	12.1	503	1	CP30_SHEEP

ALIGNMENTS

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RESULT 1
CP26_BRARE
ID CP26_BRARE STANDARD; PRT; 492 AA.
AC P79739;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
DE CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE).
GN CYP26.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094702; PubMed=8939936;
RA White J.A., Guo Y.-D., Baetz K., Beckett-Jones B., Bonasoro J.,
RA Hsu K.E., Dilworth F.J., Jones G., Petkovich M.;
RT "Identification of the retinoic acid-inducible all-trans-retinoic
RT acid 4-hydroxylase."
RL J. Biol. Chem. 271:29922-29927(1996).
CC -I- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON
CC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS
CC STEREOISOMER 9-CIS-RA. CAPABLE OF 4-HYDROXYLATION; HYDROXYLATION.
CC RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED FORMS OF RA,
CC INCLUDING 4-OH-RA AND 4-OXO-RA.
CC -I- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -I- INDUCTION: BY RETINOIC ACIDS (RA).
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
DR EMBL; U68234; AAC60045.1; -.
DR ZFIN; ZDB-GENE-990415-44; CYP26.
DR InterPro; IPR001128; -.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
KW Endoplasmic reticulum
FT BINDING 438 438 HEME (BY SIMILARITY).
SQ SEQUENCE 492 AA; 56281 MW; FD471435B2F30509 CRC64;

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Query Match 100.0%; Score 2563; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 2.9e-140;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGILYLMVTFCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPPLPGTGLPFGTETLQ 60
DB 1 MGILYLMVTFCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPPLPGTGLPFGTETLQ 60
QY 61 ILQRKFLRMKQKYGCIYKTHLFGNPTVRVMGADNVRQILLGHEKLVSVQMPASVRTL 120
DB 61 ILQRKFLRMKQKYGCIYKTHLFGNPTVRVMGADNVRQILLGHEKLVSVQMPASVRTL 120
QY 121 GSDTLNVHGVQHNKKKALMRAFSRDALEHYIPVIOQEVKSAQEWLQKDSVLYPEM 180
DB 121 GSDTLNVHGVQHNKKKALMRAFSRDALEHYIPVIOQEVKSAQEWLQKDSVLYPEM 180
QY 181 KLMFRIAMRILLGFPEQIKTDEQELVEAFEEEMIKNLFSLPIDVPFSGLYRGLRANFI 240
DB 181 KLMFRIAMRILLGFPEQIKTDEQELVEAFEEEMIKNLFSLPIDVPFSGLYRGLRANFI 240
QY 241 HSKIEENIRKKIQDDNENEQYKDALQILLIENSRSDPPSLQAMKEAATELLFGGHET 300
DB 241 HSKIEENIRKKIQDDNENEQYKDALQILLIENSRSDPPSLQAMKEAATELLFGGHET 300
QY 301 TASTATSLVPLGINTEVYQKVRREVEQKVMGMYTPGKGLSMELLQDLKYTGCVIKETL 360
DB 301 TASTATSLVPLGINTEVYQKVRREVEQKVMGMYTPGKGLSMELLQDLKYTGCVIKETL 360
QY 361 RINPVPGGFRVAKTFELNGHQIPKGNWVIYICDTHDVADVPFNKEEPQPERFMSKGL 420
DB 361 RINPVPGGFRVAKTFELNGHQIPKGNWVIYICDTHDVADVPFNKEEPQPERFMSKGL 420
QY 421 EDSGRFNYIPFGGSRMVCVKGEKFAKLLKIFLVELTQHCNLLSNGPPTMKTGPTIYVD 480
DB 421 EDSGRFNYIPFGGSRMVCVKGEKFAKLLKIFLVELTQHCNLLSNGPPTMKTGPTIYVD 480
QY 481 NLPTKFTSYVRN 492
DB 481 NLPTKFTSYVRN 492

RESULT 2
ID CP26_HUMAN STANDARD; PRT; 497 AA.
AC 043174;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
DE CYTOCHROME (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
GN CYP26A1 OR CYP26.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373542; PubMed=9228017;
RA White J.A., Beckett-Jones B., Guo Y.-D., Dillworth F.J., Bonasoro J.,
RA Jones G., Petkovich M.;
RT "cDNA cloning of human retinoic acid-metabolizing enzyme (hP450RAI)
RT identifies a novel family of cytochromes P450.";
RL J. Biol. Chem. 272:18538-18541(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98380037; PubMed=9716180;
RA Someveld E., van den Brink C.E., van der Leede B.M., Schulkes R.K.,
RA Petkovich M., van der Burg B., van der Saag P.T.;
RT "Human retinoic acid (RA) 4-hydroxylase (CYP26) is highly specific for
RT all-trans-RA and can be induced through RA receptors in human breast
RT and colon carcinoma cells.";
RL Cell Growth Differ. 9:629-637(1998).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=99045433; PubMed=9826557;
RA Trofimova-Griffin M.E., Juchau M.R.;
RT "Expression of cytochrome P450RAI (CYP26) in human fetal hepatic and

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RT cephalic tissues.";
RL Biochem. Biophys. Res. Commun. 252:487-491(1998).
CC -!- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON
CC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS
CC STEROISOMER 9-CIS-RA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-
CC HYDROXYLATION. RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED
CC FORMS OF RA, INCLUDING 4-OH-RA, 4-OXO-RA, AND 18-OH-RA.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN ADULT LIVER, HEART,
CC PITUITARY GLAND, ADRENAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.
CC -!- INDUCTION: BY RETINOIC ACIDS (RA).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; AF005418; AAB88881.1;
CC MIM; 602239;
CC InterPro; IPR001128;
CC Pfam; PF00067; P450; 1.
CC PRINTS; PR00385; P450.
CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
CC Endoplasmic reticulum.
CC BINDING 442 442 HEME (POTENTIAL).
CC SEQUENCE 497 AA; 56162 MW; EAB684B24B2EAB3 CRC64;

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Query Match 67.9%; Score 1741; DB 1; Length 497;
Best Local Similarity 68.2%; Pred. No. 3.8e-93;

Matches 339; Conservative 62; Mismatches 84; Indels 12; Gaps 5;

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QY 1 MGILYLMVTFCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPPLPGTGLPFGTETLQ 60
DB 1 MGILYLMVTFCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPPLPGTGLPFGTETLQ 60
QY 61 ILQRKFLRMKQKYGCIYKTHLFGNPTVRVMGADNVRQILLGHEKLVSVQMPASVRTL 120
DB 61 ILQRKFLRMKQKYGCIYKTHLFGNPTVRVMGADNVRQILLGHEKLVSVQMPASVRTL 120
QY 121 GSDTLNVHGVQHNKKKALMRAFSRDALEHYIPVIOQEVKSAQEWLQKDSVLYPEM 176
DB 121 GSDTLNVHGVQHNKKKALMRAFSRDALEHYIPVIOQEVKSAQEWLQKDSVLYPEM 176
QY 177 YPEVKRLMFIAMRILLGFPEQIKTDEQELVEAFEEEMIKNLFSLPIDVPFSGLYRGL 233
DB 177 YPEVKRLMFIAMRILLGFPEQIKTDEQELVEAFEEEMIKNLFSLPIDVPFSGLYRGL 233
QY 234 LRARNEIHSKTEENIRKKIQDDNENEQYKDALQILLIENSRSDPPSLQAMKEAATE 292
DB 234 LRARNEIHSKTEENIRKKIQDDNENEQYKDALQILLIENSRSDPPSLQAMKEAATE 292
QY 293 LFGGHEHTTASTATSLVPLGINTEVYQKVRREVEQKVMGMYTPGKGLSMELLQDLKY 352
DB 293 LFGGHEHTTASTATSLVPLGINTEVYQKVRREVEQKVMGMYTPGKGLSMELLQDLKY 352
QY 353 GCVIKETLRINPVPGGFRVAKTFELNGHQIPKGNWVIYICDTHDVADVPFNKEEP 412
DB 353 GCVIKETLRINPVPGGFRVAKTFELNGHQIPKGNWVIYICDTHDVADVPFNKEEP 412
QY 413 ERMSKGLSDGRSNRYTPFGGSRMVCVKGEKFAKLLKIFLVELTQHCNLLSNGPPTMKT 472
DB 413 ERMSKGLSDGRSNRYTPFGGSRMVCVKGEKFAKLLKIFLVELTQHCNLLSNGPPTMKT 472
QY 473 GPTIYVDNLPTKFTSY 489
DB 473 GPTIYVDNLPTKFTSY 489
QY 477 SPVIVPVDNLPTKFTSY 493
DB 477 SPVIVPVDNLPTKFTSY 493

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RESULT 3
CP26_MOUSE
ID CP26_MOUSE STANDARD; PRT; 497 AA.
AC O55127;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 46, Last annotation update)
DE CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
DE CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
GN CYP26A1 OR CYP26 OR P450RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=97392446; PubMed=9250660;
RA Fujii H., Sato T., Kaneko S., Gotoh O., Fujii-Kuriyama Y., Osawa K.,
RA Kato S., Hamada H.;
RT "Metabolic inactivation of retinoic acid by a novel P450
RT differentially expressed in developing mouse embryos.";
RL EMBO J. 16:4163-4173(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98113212; PubMed=9442090;
RA Abu-Abed S.S., Beckett B.R., Chiba H., Chithalen J.V., Jones G.,
RA Metzger D., Chambon P., Petkovich M.;
RT "Mouse P450RAI (CYP26) expression and retinoic acid-inducible retinoic
RT acid metabolism in f9 cells are regulated by retinoic acid receptor
RT gamma and retinoid X receptor alpha.";
RL J. Biol. Chem. 273:2409-2415(1998).
CC -!- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON
CC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS
CC STEROISOMER 9-CIS-RA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-
CC HYDROXYLATION. RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED
CC FORMS OF RA, INCLUDING 4-OH-RA, 4-OXO-RA, AND 18-OH-RA.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY RETINOIC ACIDS (RA).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC
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CC
CC -----
CC DR EMBL; Y12657; CAA73206.1; -
CC DR MGD; MGI:1096359; CYP26.
CC DR InterPro; IPR001128; -
CC DR Pfam; PF00067; P450; 1.
CC DR PRINTS; PR00385; P450.
CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
CC KW Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
CC KW Endoplasmic reticulum.
CC FT BINDING 442 442 HEME (POTENTIAL).
CC SQ SEQUENCE 497 AA; 56177 MW; 33B07D7C29134471 CRC64;

Query Match 67.7%; Score 1734; DB 1; Length 497;
Best Local Similarity 67.7%; Pred. No. 9.7e-93;
Matches 336; Conservative 61; Mismatches 89; Indels 10; Gaps 4;

QY 1 MGLYTLMTFLCTVLPVLLFLAFLKWLMLTRRVDPNCRSLPPLPGTMCGLPFIGETIQL 60
DB 1 MGLPALASALCTFVLPVLLFLAFLKWLMDLYCVSSDRSALCPPLPGTMCGLPFIGETIQL 60
QY 61 ILQRKFLMRKQKGYCIYKTHLFGNPTVRVMGADNVRQILLGHEKLVSQMPASVTRIL 120
DB 61 VLQRKFLQMKRKYGIYKTHLFGNPTVRVMGADNVRQILLGHEKLVSQMPASVTRIL 120

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QY 121 GSDTLNHNHGVQHNKKKAIMRAFSRDALEHYIPVIOQVEKSAIQENLQKDS-----VLV 176
DB 121 GACCLSNLHSDSHKQKVKVIMQAFSREALQCVLVIATAEVSVCLBQWL---SCGEGRLIV 177
QY 177 YPMKKLFRIMARILLIGPEPQI--KTDEQELVEAFEEWIKNLFESIDVPFSGLYRGL 234
DB 178 YPVKRLFRIMARILLIGCEPGAGGDEQOLVEAFEEWIKNLFESIDVPFSGLYRGL 237
QY 235 RARNFTSHKIEENIRKKIQD--DNEQEKYKDALQILLIENSRRSDEPFSLQAKKEAATL 293
DB 238 KARNLHARIEENIRKIRLQATEPDGCGCKDALQILLIENSWEGERLDMQALKQSTEL 297
QY 294 LFGHETITATSLVMFLGNTVEVQVREOVKEVMGYTPGKLSMBELDQLKYTG 353
DB 298 LFGGHETTASATSLITYLGLYPHVLOKRVREIKSKGLCKSNQDNKIDMETLEQKYIG 357
QY 354 CVIKETLRINPPVPGFRVALKTFELNGYQIPKGNVVIYSCDTHDVADVPNKEFOPE 413
DB 358 CVIKETLRINPPVPGFRVALKTFELNGYQIPKGNVVIYSCDTHDVADVPNKEFNPD 417
QY 414 REMSKLEDEGSRFNYIPFGGSRMCVKGKFAKVLKTLFVLTQHCNMIISNGPPTMKTS 473
DB 418 RFIVPHPEDASRFSEFIPFGGLRSCVKGKFAKILLKFTVELARHCDQWLINGPPTMKTS 477
QY 474 PTIYPVDNLPTKFTSY 489
DB 478 PTIYPVDNLPTKFTSY 493

RESULT 4
CS01_ARATH
ID CS01_ARATH STANDARD; PRT; 472 AA.
AC Q42569;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 90A1 (EC 1.14.-.-).
GN CYP90A1 OR CYP90 OR CPD.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=96200769; PubMed=8612270;
RA Szekeres M., Nemeth K., Konecz-Kalman Z., Mathur J., Kauschmann A.,
RA Altmann T., Redei G.P., Nagy F., Schell J., Koncz C.;
RT "Brassinosteroids rescue the deficiency of CYP90, a cytochrome P450,
RT controlling cell elongation and de-etiolation in Arabidopsis.";
RL Cell 85:171-182(1996).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC
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CC
CC -----
CC DR EMBL; X87367; CAA60793.1; -
CC DR EMBL; X87368; CAA60794.1; -
CC DR InterPro; IPR001128; -
CC DR Pfam; PF00067; P450; 2.
CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
CC KW Oxidoreductase; Monooxygenase; Heme.
CC FT BINDING 418 418 HEME (BY SIMILARITY).
CC SQ SEQUENCE 472 AA; 53785 MW; 41A73F46D64E343F CRC64;

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 CC -----

DR EMBL; AC000098; AAB71462.1; -;
 DR InterPro; IPR001128; -;
 DR Pfam; PF00067; P450.1;
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450.1;
 KW Oxidoreductase; Monooxygenase; Transmembrane; Heme.
 FT TRANSMEM 6 26 POTENTIAL.
 FT BINDING 439 439 HEME (BY SIMILARITY).
 SQ SEQUENCE 490 AA; 56409 MW; 7FD8CD7A8864D298 CRC64;

Query Match 17.6%; Score 450; DB 1; Length 490;
 Best Local Similarity 27.6%; Pred. No. 3.8e-19;
 Matches 125; Conservative 84; Mismatches 220; Indels 24; Gaps 10;

QY 41 RSLPPGTMLPFGTIGTQLLQRR-----KFLRMKQYK--CIYKTHLFGNPTVRVMG 93
 Db 42 RHYLPDGLGWPFIGNMLSLFAFKTSDPSTRTLIKRYGPKGIYKAHMFNGPSIIIVT 101
 QY 94 ADNVRLILGELHKLVSQWPSVYRTILGSDTILSNVHGQHKKKKALMRAPS-RDALEHY 152
 Db 102 SDTCRRVLTDDDAF-KPGWPTSTMLGKRSVGSFEEHKRLRLTAAPVNGHEALSTY 160
 QY 153 IPVIOQVKSATOEMKQDSCVLYPEMKKLMFRIAMRILLGPEPQIKTDQELVEAFE 212
 Db 161 IPTYEENVIVLDKTKMGEFEFL-THLKLFTIRIMYFILSSESNV--DALEREYT 216
 QY 213 EMIKNFSLPIDVPSGLYGRARNFIHSKIENIRKKIODDNEQY-----KDALQ 268
 Db 217 ALNYGVRAVATPGFAYHRAKARKTIVAAFSQSVTER---RNQKQNILSNKKDMLD 272
 QY 269 LIJENSRSDEPFSLOAMKEATELLFGGHETTASTATSLVMPGLNTEVQKVEEVOE 328
 Db 273 NILNVKDEDKTLDDLEIIDVLIMYNAGHSSGHTIMATVFLQHPHVLQRAKAE-QE 331
 QY 329 KYEMGMTPGKGLSMELLQDKYTGCVIKETLRINPPVPGGVALKTFELNGVQIPKGW 388
 Db 332 MILASREGKGLSLKETRKWEFLSQWDETLRVITSLAFREAKTDVEMNGYILPKGW 391
 QY 389 NVYISCDTHADVDPNKEEFQPERFMSKGLDGSRENYIPFGGSRMCVCKEFAVLL 448
 Db 392 KVLWFRDVIDEVPDPKRFDPARDNGFVKAGAF--LPTGAGSHLCPGNDLAKLEI 449
 QY 449 KIFLVELTQHCNWLNSNGPPTMKGTPTIYVDN 481
 Db 450 SIFLHFLKLYQVKRSNECPVWYLPHTRETDN 482

RESULT 7
 C881.MAIZE
 ID C881.MAIZE STANDARD; PRT; 519 AA.
 AC Q43246;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYTOCHROME P450 88A1 (EC 1.14.-.-) (DWARF3 PROTEIN).
 GN CYP88A1 OR D3.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
 OC Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. B73;
 RC MEDLINE=96004534; PubMed=7549486;
 RA Winkler R.G., Helentjaris T.;
 RT "The maize Dwarf3 gene encodes a cytochrome P450-mediated early step

RT in Gibberellin biosynthesis.";
 RL Plant Cell 7:1307-1317(1995).
 CC -!- PATHWAY: EARLY STEP IN GIBBERELLIN BIOSYNTHESIS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ROOTS, DEVELOPING LEAVES, THE
 CC VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; U32579; AAC49067.1; -;
 DR InterPro; IPR001128; -;
 DR Pfam; PF00067; P450.1;
 DR PROSITE; PS00086; CYTOCHROME_P450.1;
 KW Oxidoreductase; Monooxygenase; Transmembrane; Heme.
 FT TRANSMEM 1 21 POTENTIAL.
 FT BINDING 466 466 HEME (BY SIMILARITY).
 SQ SEQUENCE 519 AA; 57906 MW; 0F8977A024316D95 CRC64;

Query Match 14.6%; Score 375; DB 1; Length 519;
 Best Local Similarity 25.6%; Pred. No. 8e-15;
 Matches 119; Conservative 94; Mismatches 216; Indels 36; Gaps 13;

QY 41 RSLPPGTMLPFGTIGTQLLQRR-----KFLRMKQYK--CIYKTHLFGNPTVRVMG 93
 Db 69 RALPPGEMGPIVGGWAFRAFKSGRDPDAFTASVFRFGTGYRSFMESPTVLVTT 128
 QY 94 ADNVRLILGELHKLVSQWPSVYRTILGSDTILSNVHGQHKKK--AIMRAFSRALE 150
 Db 129 AEGCKQVLMDDDAFVT-GWPKATVALVGRSFVAMPYDEHRRIRKLTAAPINGF--DAIT 185
 QY 151 HYPTVIOQVKSATOEMKQDSCVLYPEMKKLMFRIAMRILLGPEPQIKTDQELVEA 210
 Db 186 GYLFFIDRTVTSLLRAADHGGSVFELRLRMTFKITIVQIFLG-GADQATT--RALERS 242
 QY 211 FEMIKNFSLPIDVPSGLYGR-LRARNFIHSKIENIRKKIODDNEQYK----- 264
 Db 243 YTELNGVRAVAINLP-GFAYRGALARRRLVAVLQVL-----DERRAARAKGVSGG 294
 QY 265 --DALQILIENSRSDEPFSLOAMKEATELLFGGHETTASTATSLVMPGLNTEVQK 322
 Db 295 GVDMDRLIEAQDERGRLDDDEIIDVLVIMYNAGHSSGHTIMATVFLQENPDMFARA 354
 QY 323 REEVOEKVEGMGMYTPGKGLSMELLQDKYTGCVIKETLRINPPVPGGVALKTFELNGY 382
 Db 355 KAE-QEAIMRSIPSSQRLTDRFRKMEYLSQVIDEILRLVNIISFVSFRQATRDVFNQY 413
 QY 383 QIPKGNVIYISCTDTHADVDPNKEEFQPERFMSKGLDGSRENYIPFGGSRMCVCKE 442
 Db 414 LIPKGNKVLWYRSVHMDPQVYDPDKFDPSEWEGHSPRAGT---FLAFGLGARLCPGND 470
 QY 443 FAKVLKILFELVLTQHCNWLNSNGPPTMKGTPTIYVDNLPKFT 487
 Db 471 LAKLEISVFLHFLKLYGKLTARNPCRVRLPDRVLPDNCIAKIT 515

RESULT 8
 C136.MYCTU
 ID C136.MYCTU STANDARD; PRT; 492 AA.
 AC P95099;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PUTATIVE CYTOCHROME P450 136 (EC 1.14.-.-).
 GN CYP136 OR RV3059 OR MTCY22D7.22C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;


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SQ SEQUENCE 518 AA; 59210 MW; 9B93AA12E617D0DF CRC64;

Query Match 13.7%; Score 350.5; DB 1; Length 518;
Best Local Similarity 25.6%; Pred. No. 2e-13;
Matches 112; Conservative 83; Mismatches 206; Indels 37; Gaps 10;

QY 46 PRTMGLPFGTEILQLLQRRKFLMKFKQYGYIYKTHLFGNPTVRYMGADNVROILLGE- 104
Db 40 PGPRLPFGTMTLEKKFTNFDTECFQYGRIGWIYDGRQVLCIMSKMIKTVLKEC 99
QY 105 HKLVSVQWPAVSRTILGSDTILSNVGHQHKKKAKMAFSAFSDALBHYIPVIOQE--VK 161
Db 100 YNIFTNRRNPHLNGEL-FDALSVAEEDTWRIRSVLSPTSGRLKEMFGIMKQHSSTLL 158
QY 162 SAIQEWLQKDSVLYVPEMKKLMFRIAMRL----LGFEPEQKTDQELVEAFEMIK- 216
Db 159 SGMKKQADKQDT---EVKFEFFGYSMQVTSFASVDLSLNPSPDFVSNVKKMLKF 214
QY 217 ----NLFSLEFDVPSGLYRGLARNFHSKLEE-----NIRKKIQQDDNENQKYKDALQ 268
Db 215 DLNPLLELLVAFPTGPILEKMKFSFPTAVTDFFVYASLAKIKSGROTGSTNRVDLQ 274
QY 269 LLINRSRSDPEPSLQAMK-----EATLELFGGHTTASTATSLVWFLGLNTEVVQ 320
Db 275 LMIDSGSDTKTGEBQTKGLTDHEILSQAMIFIPAGVETSSSTMSFLAYLATNHHVMT 334
QY 321 KYREEVQKVMGMYTPGKG-LSMELLDQKLTGCVIKETLRINPVPVGGFRVAKLTPEL 379
Db 335 KLEQED-----TVFPNKAPIQEAQMMDYLDVNLNESRLYPIAPRLERVAKTVETI 388
QY 380 NQYQIPKGMWVIYSICDTHDVADVPNKEFQPERFMSKGLDGSFRNFVLPFGGSRMCV 439
Db 389 NGIVIPKOCVILVPTWLRDPELWSDPEEFKPERFSKENKESIDPYTYMPEGAPRNCI 448
QY 440 GKEFAKVLKIFVLVETQ 457
Db 449 GMRFALIMIKLWVETLQ 466

RESULT 10
CP36_RABIT
ID CP36_RABIT STANDARD; PRT; 501 AA.
AC P11707; Q29306;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 3A6 (EC 1.14.14.1) (CYP11A6) (P450-3C).
GN CYP3A6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166352; PubMed=3349903;
RA Potenza C.L., Pendurthi U.R., Strom D.K., Tukey R.H., Griffin K.J.,
RT Schwab G.E., Johnson E.F.;
RT "Complete sequence of cytochrome P450 3c cDNA and presence of two
RT mRNA species with 3' untranslated regions of different lengths.";
RL DNA 7:39-46(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8938026; PubMed=2777787;
RA Potenza C.L., Pendurthi U.R., Strom D.K., Tukey R.H., Griffin K.J.,
RT Schwab G.E., Johnson E.F.;
RT "Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent
RT expression and transcriptional activation by rifampicin.";
RL J. Biol. Chem. 264:16222-16228(1989).
CC -1- FUNCTION: EXHIBITS PROGESTERONE 6 BETA-HYDROXYLASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY RIFAMPICIN.
```

```
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
Cc EMBL; M19139; AAA31430.1; -
Cc EMBL; J05034; AAA31178.1; -
Cc PIR; A29487; A29487.
Cc InterPro: IPR001128; -
Cc InterPro: IPR002397; -
Cc InterPro: IPR002401; -
Cc InterPro: IPR002402; -
Cc InterPro: IPR002403; -
Cc Pfam; PF00067; P450; 1.
Cc PRINTS; PR00359; Bp450.
Cc PRINTS; PR00385; P450.
Cc PRINTS; PR00463; EP450I.
Cc PRINTS; PR00464; EP450II.
Cc PROSITE; PS00086; CYTOCHROME_P450; 1.
Cc PROSITE; PS00465; EP450IV.
Cc Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
Cc Microsome; Endoplasmic reticulum.
Cc BINDING 440 440 HEME (BY SIMILARITY).
Cc CONFLICT 54 55 GI -> WIN (IN REF. 1).
Cc CONFLICT 165 169 GKPVD -> ASPST (IN REF. 1).
Cc CONFLICT 393 393 MISSING (IN REF. 1).
Cc CONFLICT 454 495 RD -> ES (IN REF. 1).
Cc SEQUENCE 501 AA; 57450 MW; 251D21061863ACFB CRC64;

Query Match 13.4%; Score 343.5; DB 1; Length 501;
Best Local Similarity 26.8%; Pred. No. 4.9e-13;
Matches 126; Conservative 88; Mismatches 163; Indels 93; Gaps 19;

QY 46 PGMGIPFGTEILQLLQRRK-----FLMKRQKQGYIYKTHLFGNPTVRYMGADNVROIL 101
Db 37 PGPTPLPFGI-----TILEYRKGIVDFIECRKKYKGMWGLFDGRQLMVTDPDMIKTVL 92
QY 102 LGE-----HKLVSV---OWPASVRTILGSDTILSNVGHQHKKKAL 140
Db 93 VKCYSVFTNRRSGFVGMKKAIVSDEDEW-KRVITLSP----- 133
QY 141 MRAFSRDALEHYIPVIOQE-----VKSQIQEWLQKDSVLYVPEMKKLMFRIAMRL---- 192
Db 134 --FTSGKLKEMLPITIAQYGDVLVKNLROE-AEKGKPV---DLKEIFGAYSMQVITGTS 186
QY 193 LGPEPQIKTDQELVEAFEMIKNLFSLPIDV-----PF-SGLYGLR-----ARNF 239
Db 187 FGVNIDSLRNPQDPFVKNVRRLKLSFFDPDLLSTLTLPFTPIFEALHISMFPKVVNDP 246
QY 240 IHSKIEINRKRKIQDDNENQKYK-DALQLILI--ENSRSDPEPSLQAMKEAAATE--LL 294
Db 247 LKTSVE-----KIKDRLKDKQKRRVDFTLQMLNSQNSKEIDSHKALDDIEVVAQSIIL 301
QY 295 FGGHETTASTATSLVWFLGLNTEVQKVEEVQKVMGMYTPGKGL-SMELLDQLKYKG 353
Db 302 FAGYETTSSTLSFIMHLIATHPDVQKQLEEDITLL-----PNKELATYDTLVKMEYLD 355
QY 354 CVIKETLRINPVPVGGFRVAKLTPELNGYQPKGMWVIYSICDTHDVADVPNKEEQPE 413
Db 356 MWNETLRIPYTAGLSEVRCKQKQVDINGTIFPKGTIYMWFTYALHRDPQHWTEPDERPE 415
QY 414 RFMSKGLDGSFRNFVPPGGSRMCVGEFAKVLKIFVLVETLHCHNWL 463
Db 416 RFSKKNKDNINITYHPGAGPRNCLGMRFALMKNKIALVRLMQNFSKL 465

RESULT 11
```

PCP9_HUMAN
ID CPC9_HUMAN STANDARD; PRT; 490 AA.
AC P11712;
DT 01-OCT-1989 (Rel. 12, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME P450 2C9 (EC 1.14.14.1) (CYP1C9) (P450 PB-1) (P450 MP-4)
DE (S-MEPHENYTOIN 4-HYDROXYLASE) (P-450MP).
GN CYP2C9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=68103561; PubMed=2827463;
RA Meenan R.N., Gosland J.R., Ront D., Hastie N.D., Friedberg T.,
RA Adesnik M., Buckland R., van Heyningen V., Fletcher J., Spurr N.K.,
RA Sweeney J., Wolf C.R.;
RT "Human cytochrome P-450 PB-1: a multigene family involved in
RT mephenytoin and steroid oxidations that maps to chromosome 10.";
RL Am. J. Hum. Genet. 42:26-37(1988).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=88096500; PubMed=3697070;
RA Kimura S., Pastewka J., Gelboin H.V., Gonzalez F.J.;
RT "cDNA and amino acid sequences of two members of the human P450IIC
RT gene subfamily.";
RL Nucleic Acids Res. 15:10053-10054(1987).
RN [3]
RN SEQUENCE OF 108-490 FROM N.A.
RX MEDLINE=89062423; PubMed=3196692;
RA Ged C., Unbehauer D.R., Bellow T.M., Bork R.W., Srivastava P.K.,
RA Shiraki N., Lloyd R.S., Guengerich F.P.;
RT "Characterization of cDNAs, mRNAs, and proteins related to human
RT liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase.";
RL Biochemistry 27:6929-6940(1988).
RN [4]
RN VARIANTS.
RX MEDLINE=97101957; PubMed=8946475;
RA Stubbins M.J., Harries I.W., Smith G., Tarbit M.H., Wolf C.R.;
RT "Genetic analysis of the human cytochrome P450 CYP2C9 locus.";
RL Pharmacogenetics 6:429-439(1996).
RN [5]
RN VARIANTS.
RX MEDLINE=97264536; PubMed=9110362;
RA Blasker C.R., Miners J.O., Coulter S., Birkett D.J.;
RT "Allelic and functional variability of cytochrome P4502C9.";
RL Pharmacogenetics 7:51-58(1997).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY RIFAMPIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -!- DATABASE: NAME-Cytochrome P450 Allele Nomenclature Committee;
CC NOTE-CYP2C9 alleles;
CC WWW="http://www.imm.ki.se/CYPalleles/cyp2c9.htm".
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CC -----
DR EMBL; M21940; AAA52159.1; -.
DR PIR; A28530; A28530.

DR PIR; S06863; S06863.
DR MIN; G01130; -.
DR InterPro; IPR001128; -.
DR InterPro; IPR002397; -.
DR InterPro; IPR002401; -.
DR InterPro; IPR002403; -.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00359; BP450.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00463; BP450I.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Polymorphism.
FT BINDING 435 435 HEME (BY SIMILARITY).
FT VARIANT 144 144 R -> C (IN CYP2C9*2).
FT VARIANT 358 358 Y -> C.
FT VARIANT 417 417 /FTID=VAR_008344.
FT VARIANT 359 359 I -> L (IN CYP2C9*3; RESPONSIBLE FOR THE
FT TOLBUTAMIDE POOR METABOLIZER PHENOTYPE).
FT VARIANT 417 417 /FTID=VAR_008345.
FT VARIANT 417 417 G -> D.
FT CONFLICT 4 4 /FTID=VAR_008346.
FT CONFLICT 175 175 L -> I (IN REF. 2).
FT CONFLICT 239 239 C -> Y (IN REF. 1).
FT CONFLICT 239 239 F -> L (IN REF. 1).
SQ SEQUENCE 490 AA; 55627 MW; 4FDFC395303M4E3E CRC64;

Query Match 13.2%; Score 339.5; DB 1; Length 490;

Best Local Similarity 26.9%; Pred. No. 8.1e-13;

Matches 139; Conservative 83; Mismatches 218; Indels 77; Gaps 22;

QY 5 TLMVTFCLTIVLPVLLFLAAVAKLWMLIRVDNCRSLPPTGTLGTFIGETLQL-ILQ 63
DB 3 SLVVLVIC---LSCILLLS---LWR-----QSSGRGKLPPGPTLPVIGNILQIGIKD 49
QY 64 RRKFLRMKQKYCIYKTHLFGNPTVRVMGADNVRQIL--LGEHKLVSQVMPASVITIG 121
DB 50 ISKSLINLKVYGVPTLYLGLAPVILVHGYEAVKEALIDLGEFSGRGIFPLAERANG 109
QY 122 SDTSLNVHGVQEKKKK-AIMRAFSDALEHYIPVIOQEVKSAIQEWLQKDSVLYPEM 180
DB 110 -----FGIVFSNGKKWEIRRFSLMTRNF-----GMGKRSIEDRVQEEARCLVEELR 157
QY 181 KKLFRIMRILLGFEPEQI-----KTDEQ--ELVEAFBEMIK-----N 217
DB 158 KTKASPCDPTFTILGAPCNVICSIFPKRFYKQOQFLNMEKLNENIKILSPWIOICN 217
QY 218 LFLSLPDPVPSGLYRGLRARN--FIHSKTEENIRKKIQQDDNENEQYKDALQLLIENS 275
DB 218 NFSPIDY-FPGTHNKL-LKNVAFMSYILEKVEHQESMDMNNPQDFIDCFMKMEKEK 275
QY 276 RSD-EPPSLQAMKEAATLFLGGHETATSTASTATSLVMTGLNTEVWVKYREVEQKVEGM 334
DB 276 HNOFSEFTIESLNTAVDLFGAGTETTTLLRYALLLLKHPVETAKVQEEIERVI----- 331
QY 335 YTPCKGLS--MELLDLQKYGCYVKETILNPPNPPGGFRVALK-TFELNGYQIPKGNVI 391
DB 332 ---GRNRCMCDRSHMPTDAVVHEVQRYIDLLTSLPFAVTCIDIKFRNLIPIKPGTIL 388
QY 392 YSICDT-HVADVDFNKEFQEPREFRMSKGLDGSGREN----YIPEGGSGCMCVKEFAKY 446
DB 369 ISLTSVLHUNKE-FPNPDMFDPHF---LDGGNFKKSKYFNPFSAGKRICVGEALAGM 443
QY 447 LKFLVELTQHCNWLNSGPTMTKPTIYFVNLP 483.
DB 444 ELFLFLTSLIQNFNLKSLVDPKNDITTPVNGFASVP 480

RESULT 12
CPCA_HUMAN


```

RT Anabaena sp. strain PCC 7120 nifD element.";
RL J. Bacteriol. 172:6981-6990(1990).
RN [2]
RN REVISIONS.
RP Lammers P.J., Trujillo-Provencio C., Sanchez C., Carillo M.;
RA Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL
CC CC -!- FUNCTION: PROBABLY INVOLVED IN ALKANE/PARTY ACID HYDROXYLASE.
CC CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; U98537; AAC82967.1; -.
CC CC PIR; C37842; C37842.
CC CC InterPro; IPR001128; -.
CC CC Pfam; PF00067; p450; 1.
CC CC PRINTS; PR00385; P450.
CC CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC CC oxidoreductase; Monooxygenase; Electron transport; Heme;
CC CC Nitrogen fixation.
CC CC BINDING 393 393 HEME (BY SIMILARITY).
CC CC SEQUENCE 459 AA; 552525 MW; 67C62908C94C5698 CRC64;
CC CC FT

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Search completed: November 6, 2001, 13:39:39
Job time: 242 sec

us-09-668-482-2.rsp

Wed Nov 7 09:29:14 2001